

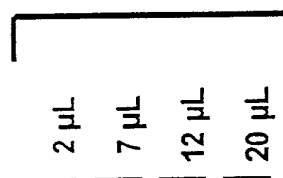
atg gca agt cca gag cac cct ggg agc cct ggc tgc atg gga ccc ata	48
Met Ala Ser Pro Glu His Pro Gly Ser Pro Gly Cys Met Gly Pro Ile	
1 5 10 15	
acc cag tgc acg gca agg acc cag cag gaa gca cca gcc act ggc ccc	96
Thr Gln Cys Thr Ala Arg Thr Gln Gln Glu Ala Pro Ala Thr Gly Pro	
20 25 30	
gac ctc ccg cac cca gga cct gac ggg cac tta gac aca cac agt ggc	144
Asp Leu Pro His Pro Gly Pro Asp Gly His Leu Asp Thr His Ser Gly	
35 40 45	
ctg agc tcc aac tcc agc atg acc acg cgg gag ctt cag cag tac tgg	192
Leu Ser Ser Asn Ser Ser Met Thr Thr Arg Glu Leu Gln Gln Tyr Trp	
50 55 60	
cag aac cag aaa tgc cgc tgg aag cac gtc aaa ctg ctc ttt gag atc	240
Gln Asn Gln Lys Cys Arg Trp Lys His Val Lys Leu Leu Phe Glu Ile	
65 70 75 80	
gct tca gct cgc atc gag gag aga aaa gtc tct aag ttt gtg gtg tac	288
Ala Ser Ala Arg Ile Glu Glu Arg Lys Val Ser Lys Phe Val Val Tyr	
85 90 95	
caa atc atc gtc atc cag act ggg agc ttt gac aac aac aag gcc gtc	336
Gln Ile Ile Val Ile Gln Thr Gly Ser Phe Asp Asn Asn Lys Ala Val	
100 105 110	
ctg gaa cgg cgc tat tcc gac ttc gcg aag ctc cag aaa gcg ctg ctg	384
Leu Glu Arg Arg Tyr Ser Asp Phe Ala Lys Leu Gln Lys Ala Leu Leu	
115 120 125	
aag acg ttc agg gag gag atc gaa gac gtg gag ttt ccc agg aag cac	432
Lys Thr Phe Arg Glu Glu Ile Glu Asp Val Glu Phe Pro Arg Lys His	
130 135 140	
ctg act ggg aac ttc gct gag gag atg atc tgt gag cgt cgg cgc gcc	480
Leu Thr Gly Asn Phe Ala Glu Glu Met Ile Cys Glu Arg Arg Arg Ala	
145 150 155 160	
ctg cag gag tac ctg ggc ctg ctc tac gcc atc cgc tgc gtg cgc cgc	528
Leu Gln Glu Tyr Leu Gly Leu Leu Tyr Ala Ile Arg Cys Val Arg Arg	
165 170 175	
tcc cgg gag ttc ctg gac ttc ctc acg cgg ccg gag ctg cgc gag gct	576
Ser Arg Glu Phe Leu Asp Phe Leu Thr Arg Pro Glu Leu Arg Glu Ala	
180 185 190	
ttc ggc tgc ctg cgg gcc ggc cag tac ccg cgc gcc ctg gag ctg ctg	624
Phe Gly Cys Leu Arg Ala Gly Gln Tyr Pro Arg Ala Leu Glu Leu Leu	
195 200 205	
ctg cgc gtg ctg ccg ctg cag gag aag ctc acc gcc cac tgc cct gcg	672
Leu Arg Val Leu Pro Leu Gln Glu Lys Leu Thr Ala His Cys Pro Ala	
210 215 220	
gcc gcc gtc ccg gcc ctg tgc gcc gtg ctg ctg tgc cac cgc gac ctc	720
Ala Ala Val Pro Ala Leu Cys Ala Val Leu Cys His Arg Asp Leu	
225 230 235 240	

FIGURE 1

gac cgc ccc gcc gag gcc ttc gcg gcc gga gag agg gcc ctg cag cgc	768
Asp Arg Pro Ala Glu Ala Phe Ala Ala Gly Glu Arg Ala Leu Gln Arg	
245 250 255	
ctg cag gcc cgg gag ggc cat cgc tac tat gcg cct ctg ctg gac gcc	816
Leu Gln Ala Arg Glu Gly His Arg Tyr Tyr Ala Pro Leu Leu Asp Ala	
260 265 270	
atg gtc cgc ctg gcc tac gcg ctg ggc aag gac ttc gtg act ctg cag	864
Met Val Arg Leu Ala Tyr Ala Leu Gly Lys Asp Phe Val Thr Leu Gln	
275 280 285	
gag agg ctg gag gag agc cag ctc cgg agg ccc acg ccc cga ggc atc	912
Glu Arg Leu Glu Glu Ser Gln Leu Arg Arg Pro Thr Pro Arg Gly Ile	
290 295 300	
acc ctg aag gag ctc act gtg cga gaa tac ctg cac tga	951
Thr Leu Lys Glu Leu Thr Val Arg Glu Tyr Leu His	
305 310 315	

FIGURE 1 cont'd

Cell Lysate



kDa

250 —

148 —

60 —

42 —

30 —

22 —

17 —

6 —

4 —

FIGURE 2

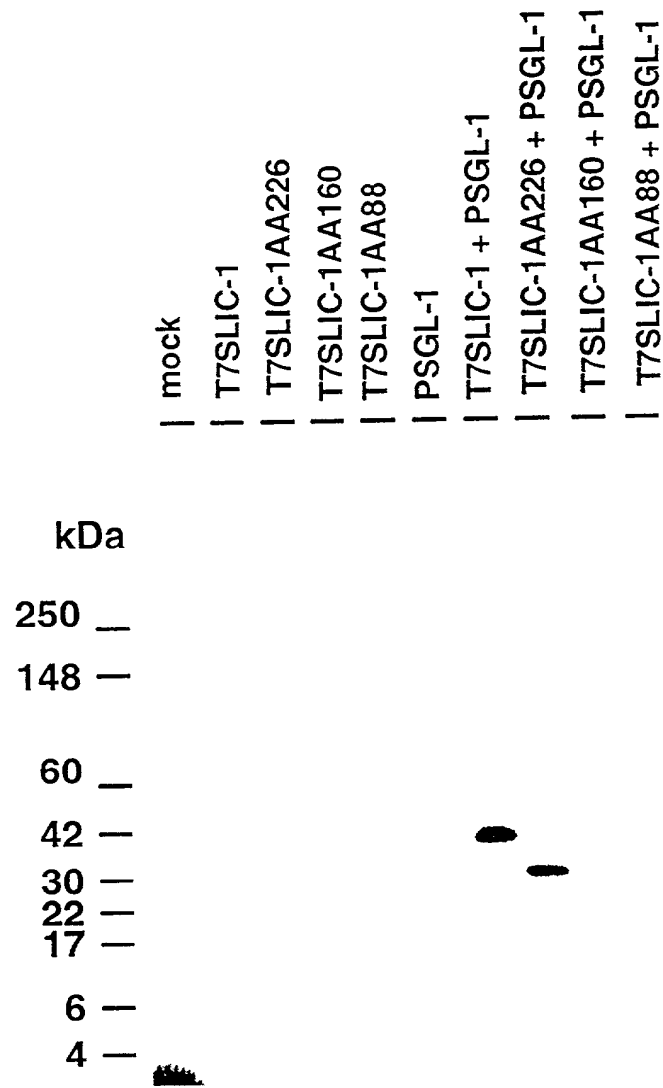


FIGURE 3

Genomic exon-intron boundary structure of the human SLIC-1 gene

Exon 1 - GAGACTGGAG -86 87- CCTTGGAGCA - EXON 2
 |||||
 GAGACTGGAGgtcagtattt cctctggcagCCTTGGAGCA
 Intron 1 (3651bp)

Exon 2 - CGGGCACCTTA -224 225- ACACACACAG - EXON 3
 |||||
 CGGGCACCTTAgtgggctt gtccttccagACACACACAG
 Intron 2 (1474bp)

Exon 3 - TAAGTTTGTG -377 378- GTGTACCAAA - EXON 4
 |||||
 TAAGTTTGTGgtaagcagag tggccctagGTGTACCAAA
 Intron 3 (1695bp)

Genomic exon-intron boundary structure of the mouse SLIC-1 gene

Exon 1 - TCCCAGGTCA CCTTGGAGCA - EXON 2
 |||||
 TCCCAGGTCAgtcagtgttt gctcaggtagCCTTGGAGCA
 Intron 1

Exon 2 - GGATCAGAAA CTCAGGTAGC - EXON 3
 |||||
 GGATCAGAAAggtaaaactgg ctctttagCTCAGGTAGC
 Intron 2

Exon 3 - CAAGTTTGTG ATGTACCAAG - EXON 4
 |||||
 CAAGTTTGTGgtaagcagag ctgctgcagATGTACCAAG
 Intron 3

FIGURE 4